

NEW_SEQLIST.ST25.txt
SEQUENCE LISTING

<110> Shen, Ben

<120> Methods of directing C-O bond formation utilizing a type II polyketide synthase system

<130> 054030-0031

<140> 10/646,664

<141> 2003-08-22

<150> 60/405,245

<151> 2002-08-22

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 15559

<212> DNA

<213> Streptomyces griseus

<400> 1

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| tgaccgcgc | gatcgaccgg | tccccgact | accgggtcga | gaagcccga | cttctcctct | 10380 |
| gcggtgaaca | cgacagcacg | ggtaacatcc | gctcggcgat | ggaacggtgg | agcgaacgcg | 10440 |
| atccccacag | cgagttccat | gtgatccccg | gtgccggaca | tgctcgcaat | ctggaccgtc | 10500 |
| ccgacgaggt | caaccggctg | accgtcgcct | tcctgaaggc | ctgagacccc | agcgagacca | 10560 |
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NEW_SEQLIST.ST25.txt

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| tcccgcaggc | caccggccgc | ctcttcggct | acctcctgct | gcgcaacaag | ccggtggacc | 10740 |
| tcgacaccat | gacccgcgaa | ctcggccagg | ccaagagcgg | gctgagtgtg | gccgcccgcc | 10800 |
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| acgaggcggg | gggagacctc | cagcacctgc | tgctggtgaa | caacgcccac | atgcgcaagt | 10920 |
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| gggaggcccc | gcgcgccgcc | acctgagccc | ggccgttccc | ttctcccttc | tgagcccggc | 11100 |
| cgttctcttc | tccctccttc | tccgcttctt | cgtccttccc | cttcctgctt | ccgatggagt | 11160 |
| gaccgtgaac | gtgtcgtccg | tccccgcgcc | gggcaacgga | acaacggtgg | ccaccgccgt | 11220 |
| ggcggaccct | ggagtccgga | tccgcccgcc | ggtcatggac | gcctgctcgc | tgggtgtacga | 11280 |
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| tgtcttctcc | gcctcgttct | gccggtactt | cggcgccctg | cacaccgcgt | accgcgacgc | 11400 |
| gctcgccgtc | cgccggcagg | acgcgatcga | cgtgctcctg | ccaccggacc | ggccaccggt | 11460 |
| cgatctggcc | gggcatctcg | cggaccggga | acggcagggt | gtgacgggag | agttcgccat | 11520 |
| gggctcggcg | gaacggctgc | cggacggccg | tacggtcaac | gagtggctgc | tggagaccgt | 11580 |
| acgggacgtg | cgcgaccgga | tccacgtctg | ggccgggata | tccctgcgcg | accccgccgc | 11640 |
| cgcgctgcgg | gagctggagc | ggctcgtggc | ggccggggcg | accgggctgt | gcgtcatccc | 11700 |
| cttcctggac | ggcaccgacc | cggccgaccc | gaggttcgcc | ccggtctggg | acgccgcggc | 11760 |
| cgaggcgcg | ctgccggtct | ggctgcacac | cggccaccac | ttcgcccgga | gccaccccag | 11820 |
| cggcctgggc | agctggcgta | cggtcgagac | gctcgcgggc | cgccaccgcg | cgctgctgct | 11880 |
| cgtcgccggg | cacgcgggct | ggcccgatgt | gcaggagatg | ctgctcacgg | ccgcccgga | 11940 |
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| ccgtcgccgg | gggcagggga | tccgccggac | ggccgaaagc | cgcagccccg | tcggaagcct | 12300 |
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| gtcagccacc | ccgaccaacg | gagatgtacg | acatggcaaa | gatccttttc | gtggtgtccg | 12420 |
| gcgcggacca | ctggaccctg | gcggacggca | cggcccaccc | cacgggcttc | tgggcccagg | 12480 |

NEW_SEQLIST.ST25.txt

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| cgggcggtgt | cgtcccgacc | gtggaccggg | gcagcctggc | gcccgcgctc | aacggcgggc | 12600 |
| aggagggcgc | cgacgcggtg | gcggccgggtc | ttgagggcgtt | cgaggagctg | cggcgggccg | 12660 |
| tcgccctgga | ggacgtggac | ccggacgtgt | acgacgccgt | cttctacccc | ggcgggccacg | 12720 |
| gcccgatgga | ggacctcgcg | gtggaccccc | tctccggggc | gctgctcgcc | cgggtgctgg | 12780 |
| cttcgggcaa | gccgctcggc | gtggtctgcc | acggcccggc | ggcgctgctg | gccgcgaccg | 12840 |
| gacccgacgg | ccggtccgcg | ttcgccgggt | atcggtgac | gggcttcacc | aacgccgagg | 12900 |
| aggcccaggc | gggcttcgcg | gacaaggcga | agtggctgct | ccaggaccgg | ctggtggcgc | 12960 |
| tgggcgcgga | cttcaggaa | ggtgagccct | gggcgcggtt | cgatcatcacc | gaccggaacc | 13020 |
| tgatcacggg | tcagaacccg | gcctcctccg | tcccgttggc | cgccgaactg | ctcaaccggc | 13080 |
| tcggctgacc | ggccgatcgg | cggttcgccg | cccggccggc | cgggctgttc | agaccagtc | 13140 |
| ccgccgcgcg | ggcggtcgc | agagctccag | caccaccgcg | cccgtctcgg | gctcgtcccc | 13200 |
| ggagacgggc | cggacgcgcg | caccgaccgt | caccaggtgc | ggagccgccc | ccacgatctg | 13260 |
| gcagcggaag | acgaaccctt | ccgagaaccg | caccagggac | tcgttgcgcg | cagcctcggt | 13320 |
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| cagttcgctc | gacgcgcaca | ccgggcacag | cagccgccgg | aacgaggcgg | tgccgcacca | 13440 |
| gcggcagcga | ttgtaggaga | ggccgcactc | ctcgtgcgcc | ttctggacgg | tgccattgac | 13500 |
| tgtctgggac | acggctcgac | cccctgcgct | cgactcggac | gcgccgcacc | tgcactgcgg | 13560 |
| gcgcgtccgc | accatatggc | actcagtgcc | ggaccgtaaa | ggcactgagt | gcccattggt | 13620 |
| actcagttct | cgccgacggc | tgcttcgatc | tgctgcacga | cacgccacat | cgggggtgccc | 13680 |
| ttccgcgcga | ccatcacgat | cacctccctt | ttcccgctgc | cgccaccgga | gaccggaaag | 13740 |
| gggggtggccg | gtgtggggac | ggcaggccgc | ccccacacct | ctcggaccag | ggcgagcgca | 13800 |
| tgatccacag | ccgcctcggg | gtcgcccgcc | ccgcccgaac | gcagccacag | ccgaagcccg | 13860 |
| ttgtttgtgcg | cggcgaccac | cgaagcggcg | atcacctcgg | cccgcagctc | cccgtcgcga | 13920 |
| ccctcgccga | agcgaccccc | cagatgtccg | gcgagagtct | gttcgtaacg | gcgcaccacc | 13980 |
| gacagttcgt | acgtccgcag | ccccggcacc | tcccagagtga | ggcggtagcg | ctgcacggag | 14040 |
| aactcgggggt | tggccgcgta | catccgcagc | acgatgcgcg | cggcgctcga | caccgcgccg | 14100 |
| accgggtcgc | tgctcgtcgac | ggcgggccagg | aactcggctg | tctcggcgag | gcagcgctcg | 14160 |
| tgggtccggga | agaccgcgtc | ctccttggac | gggaagtagc | ggaagaacga | acgccggccc | 14220 |
| accccgccca | gcgccacgat | gtcgtccacg | gtcgtccgct | cgaagccccg | ctccaggaag | 14280 |
| agccggaagg | ccgcctgtgc | gagcacctcc | cgcattgggtg | ccttcttctc | ggatcctcgc | 14340 |
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NEW_SEQLIST.ST25.txt

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| accaggttag | gcaggagagc | cggcgtgagc | ttgaggatcg | ttgtctgtgt | gaagtacgtg | 14520 |
| cccgacgcga | ccggtgaccg | gcgtttcgcc | gatgacctga | cgctggaccg | tgaggatgtc | 14580 |
| gacggtctgt | tgtcggagct | ggacgagtac | gcggtcgagc | aggcgttgca | gatcgctgac | 14640 |
| ggggcggacg | atgcggagat | caccgtggtg | acggtgggtc | cggaggatgc | caaggacgcg | 14700 |
| ttgcgcaagg | cgttgctgat | gggtgcggac | aaggcggttc | acgtcgagga | cgacgatctg | 14760 |
| cacggcagtg | atgtgatggg | gacgtcgctg | gtgctggcga | aggctgtgga | gaaggccggg | 14820 |
| tatgacctgg | tgatctgtgg | gatggcgctg | acggacggtg | tgatgggtgt | gctgccggcg | 14880 |
| ttgctggcgg | agcgtctggg | tgtgccgcag | gtgacgttgc | tgtccgaggt | cgcggtggac | 14940 |
| ggtggtgtgg | tgacggggcg | gcgtgacggt | gacacggcgt | ccgagcagct | tgaggcgctg | 15000 |
| cttcccgcgg | tgggtgtcgg | gaccgaccag | tcgggtgagg | cccgttacct | gtcgttcaag | 15060 |
| gggatcatgg | cggcgaagaa | gaagccggtg | gagtcgctgg | acctggacga | tctgggtctg | 15120 |
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| cacggtgcgg | tgaaggtcct | gacctcggac | gccccggagt | tcgcggatta | tctggtggtg | 15540 |
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 <212> DNA
 <213> STREPTOMYCES GRISEUS

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| gacggccgcg | cctgcaccga | cctggacacc | ttctgggggtg | tggtgcgcga | cggggcgagc | 120 |
| tgctctctcc | cgtacgcca | tcccgaactc | cccctccgta | tcgccgggac | cgtgaacggc | 180 |
| tgggacccgg | agaccgaact | cccgtgtcgt | gaacggcaga | tacgccgttc | ctcgcgcgcc | 240 |
| gggctgatgg | ccacgggtgc | ggtgcaccgg | gcgctggagc | acgccgggct | gagcgcggac | 300 |
| gacctcgatc | cggggcgctac | cgcgctcgtc | gcctgctcgc | tccagttcgc | gttcccggag | 360 |
| accgagcgct | actacgccct | ggcccgggac | gaggggggtcg | ccgccctcgg | catggagtac | 420 |
| tggctcaacg | ggaccccgcc | cagtgtgggtg | ggcaccgtgg | cctccggcct | ccggctgccc | 480 |

NEW_SEQLIST.ST25.txt

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<210> 3
<211> 426
<212> PRT
<213> Streptomyces griseus
<400> 3

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Leu Pro Gly Pro Asp Gly Arg Ala Cys Thr Asp Leu Asp Thr Phe Trp
          20          25          30

Gly Val Val Arg Asp Gly Ala Ser Cys Leu Ser Pro Tyr Ala His Pro
          35          40          45

Glu Leu Pro Leu Arg Ile Ala Gly Thr Val Asn Gly Trp Asp Pro Glu
50          55          60

Thr Glu Leu Pro Leu Ser Glu Arg Gln Ile Arg Arg Ser Ser Arg Ala
65          70          75          80

Gly Leu Met Ala Thr Gly Ala Val His Arg Ala Leu Glu His Ala Gly
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Leu Ser Ala Asp Asp Leu Asp Pro Gly Arg Thr Ala Leu Val Ala Cys
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NEW_SEQLIST.ST25.txt

Ser Leu Gln Phe Ala Phe Pro Glu Thr Glu Arg Tyr Tyr Ala Leu Ala
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Arg Asp Glu Gly Val Ala Ala Leu Gly Met Glu Tyr Trp Leu Asn Gly
130 135 140

Thr Pro Pro Ser Val Val Gly Thr Val Ala Ser Gly Leu Arg Leu Pro
145 150 155 160

Cys Gln Thr Leu Ser Val Ala Gly Ser Cys Asn Val Ala Leu Arg Thr
165 170 175

Leu His Leu Val Gln Gln Met Phe Arg Cys Gly Asp Ile Asp Arg Ala
180 185 190

Ile Val Val Gly Val Asp Thr Thr Val Asp Pro Val Phe Val Ala Gly
195 200 205

Thr Ser His Thr Gly Arg Ser Gly Tyr Arg Ala Ser Ser Leu Ser Asp
210 215 220

Asp Pro Ala Asp Val Arg Pro His Asp Glu Ile Gln Thr Gly Asn Ala
225 230 235 240

Thr Gly Glu Gly Ala Leu Ala Val Val Leu Glu Asn Pro Ala Ala Thr
245 250 255

Gly Asp Arg Pro Gly Leu Leu His Arg Ala His Leu Arg Thr Ser Arg
260 265 270

Ser Asn Gly Pro Ser Thr Val Ala Thr Gly Pro Pro Ala Asn Val Val
275 280 285

Gly Asp Val Leu Ala Thr Leu Ala Ser Ala Arg Arg Gly Leu Gly Asp
290 295 300

Leu Ala Phe Val Asn Asp Tyr Ala Asp Gly Asn Arg Phe Val Glu Asp
305 310 315 320

His Leu Cys Gln Ala Leu Ala Gly Val Lys Glu Ala Ala Gly Tyr Gly
325 330 335

Gly Glu Leu Arg Leu Thr Asn Gln Glu Ala Val Phe Gly His Val Ala
340 345 350

Gly Thr Gly Gly Leu Val Lys Leu Leu Gly Ser Leu Leu Met Leu Arg

355

360

365

His Gly His Ile Ala Pro Ser Ala Asn Thr Leu Val Pro Tyr Ala Gly
 370 375 380

Leu Pro Gly Asp Pro Val Leu Ala Gly Gly Leu Ala Thr Gly Gly Asp
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Ser Ala Leu Val Leu Ala Ser Gly Ala Gly Gly Asp Ala Thr Ser Met
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Val Ile Glu Tyr Glu Gly Gly Asp Leu Pro
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<211> 1278

<212> DNA

<213> Streptomyces griseus

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NEW_SEQLIST.ST25.txt

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<211> 425
<212> PRT
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<400> 5

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Asp Gly Phe His His Gly Thr Val Arg Gly Ala Arg Glu Ala Phe Gly
35 40 45

Glu Leu Leu Pro Asp Ile Pro Ala Arg Tyr Leu Arg Ser Tyr Ala Asp
50 55 60

Val His Leu Tyr Gly Leu Ile Ser Leu Ala Glu Ala Cys Arg Asp Ala
65 70 75 80

Gly Leu Asp Tyr Gly Lys Gly Glu Leu Arg Gly Ala Asp Val Leu Thr
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Ala Arg Ala Gly Val Asp Ser Asn Tyr Asp Ser Tyr Arg Ala Trp His
100 105 110

Asp Ala Asp Pro Ala Thr Val Thr Pro Ser Asp Ala Lys Ser Leu Phe
115 120 125

Val Arg Leu Leu Val Ala Gly Thr Ser Ser Asp Val Gly Pro Val Gln
130 135 140

Ala Ala Leu Leu Gly Ser Thr Gly Ala Asn Tyr Thr Val Ser Cys Gly
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Cys Ala Ser Ser Ser Val Leu Leu Gly Ile Ala Arg Met Met Ile Ala
165 170 175

Ser Gly Gln Ser Asp Leu Val Val Val Thr Gly Val Asp Arg Phe Asp
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Thr Glu Arg Val Leu His Gly His Arg Leu Arg Glu Val Val Glu Arg

195

200

205

Glu Gly Val Thr Val Arg His Asn Ser Asp Pro Pro Ala Ala Pro Arg
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 His Asp Arg Pro Met Arg Pro Tyr Asp Ala Ala Gly Asp Cys Met Asn
 225 230 235 240
 Tyr Gly Asp Gly Ser Val Thr Leu Ile Leu Glu Ser Arg Glu His Ala
 245 250 255
 Ala Ala Arg Gly Ala Arg Thr His Gly Ala Val Leu Gly Gln Ala Thr
 260 265 270
 Thr Arg Gly Gly Leu Asn Ser Ala Val Ala Ile Asp Thr Gly Gly Thr
 275 280 285
 Gly Leu Ala Glu Ala Ala Arg Arg Ala Leu Gly Asp His Thr Ser Leu
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 Gly Arg Ile Pro Tyr Val Asn Gly Gly Gly Glu Gly Asp Ala Leu Phe
 305 310 315 320
 Thr Arg Ile Glu Ser Asn Ala Val Arg Ala Leu Trp Gly Asp Arg Ser
 325 330 335
 Glu Gln Val Leu Val Ser Ser Gln Glu Ala Cys Phe Gly His Ser Gly
 340 345 350
 Ala Pro Leu Gly Asn Leu Gly Thr Ala Leu Thr Leu Met Met Met Arg
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 Glu Gly Glu Val Cys Pro Thr Ala Asn Cys Ala Thr Pro Ser Pro Val
 370 375 380
 Cys Thr Phe Asp Pro Val Pro Gly Thr Arg Thr Arg Ala Leu Gly Phe
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 <211> 1658
 <212> DNA
 <213> Streptomyces griseus

NEW_SEQLIST.ST25.txt

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ggttcgggggt cccgggtccgc gcgctgttca acatgaccga ggtgtcgtgt ccggtgctct 1020
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<210> 7
<211> 555
<212> PRT
<213> Streptomyces griseus

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NEW_SEQLIST.ST25.txt

<400> 7

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Glu Gln Cys Val Leu Gly Pro Leu Leu Arg Arg Arg Ala Ala Ala Ala
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Pro Ala Ala Pro Tyr Ala Leu Met Pro Asp Gly Asp Leu Trp Thr Tyr
35     40     45

Ala Arg Thr Leu Arg Glu Thr Glu Glu Thr Ala Ala Ala Leu Gln Ala
50     55     60

Leu Gly Val Val Pro Gly Glu Leu Val Leu Ser Trp Leu Pro Asn Gly
65     70     75     80

Pro Asp Ala Leu Arg Ala Trp Tyr Gly Val Asn Leu Ala Gly Ala Val
85     90     95

Leu Val Pro Leu Asn Ile Ala Tyr Arg Gly Ala Ile Leu Arg Gln Val
100    105    110

Ile Ala Asp Ser Gly Ala Glu Val Leu Ile Cys Arg Pro Ser Leu Ala
115    120    125

Ala Arg Leu Glu Asp Ser Asp Asp Ala Val Gly Ala Val Arg Thr Val
130    135    140

Val Leu Leu Pro Gly Pro Glu Asp Ala Ala Gln Asp Val Glu Ala Leu
145    150    155    160

Ala Gly Arg Leu Ala Thr Arg Phe Arg Val Glu Thr Ala Leu Arg Ala
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Asp Arg Ala Glu Phe Ala Glu Pro Val Pro Ala Pro Arg Pro Trp Asp
180    185    190

Pro Gln Thr Val Ile Tyr Thr Ser Gly Thr Thr Gly Pro Ser Lys Gly
195    200    205

Val Val Ser Ser Tyr Ala His Leu Tyr Ser Ser Cys Thr Ala Ala Phe
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His Gly Met Ala Gly Pro Glu Asp Arg Tyr Leu Leu Gln Leu Pro Leu
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Phe His Ala Gly Gly Thr Ile Gly Ala Tyr Gly Met Leu Val His Gly
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 Gly Ser Val Thr Val Val Pro Ala Phe Thr Thr Gly Glu Phe Trp Pro
 260 265 270
 Leu Ile Arg Arg Thr Gly Thr Thr Leu Cys Thr Leu Leu Gly Val Met
 275 280 285
 Ala Thr Tyr Leu Leu Lys Gln Pro Pro Leu Pro Gln Asp Thr Ala His
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 Pro Leu Arg Ala Ala Tyr Val Ile Pro Phe Thr Glu Gly Ala Thr Glu
 305 310 315 320
 Phe Ser Lys Arg Phe Gly Val Pro Val Arg Ala Leu Phe Asn Met Thr
 325 330 335
 Glu Val Ser Cys Pro Val Leu Ser Ala Pro Asp His His Pro Gly Val
 340 345 350
 Pro Met His Cys Gly Glu Pro Arg Pro Gly Ile Ala Ala Arg Val Val
 355 360 365
 Asp Asp His Asp Arg Glu Val Ala Asp Gly Glu Ala Gly Glu Leu Val
 370 375 380
 Leu Arg Ala Asp Arg Pro Trp Ser Phe Leu Ser Gly Tyr Leu Gly Arg
 385 390 395 400
 Pro Ala Glu Thr Ala Ala Val Trp Arg Asn Gly Trp Phe His Thr Gly
 405 410 415
 Asp Thr Phe Arg Arg Ala Pro Asp Gly Gly Leu Val Phe Val Asp Arg
 420 425 430
 Lys Lys Asp Ala Ile Arg Arg Arg Gly Glu Asn Ile Ser Ser Phe Glu
 435 440 445
 Val Glu Ala Gln Ala Val Ala His Pro Gly Val Leu Glu Ala Ala Ala
 450 455 460
 Val Ala Val Pro Gly Asp Glu Gly Glu Asp Glu Val Leu Leu Val Val
 465 470 475 480
 Ala Asp Arg Asp Pro Ser Ala Pro Val Asp Pro Ala Ala Leu Leu Glu
 485 490 495

NEW_SEQLIST.ST25.txt

Phe Leu Arg Glu Arg Leu Ala His Phe Met Leu Pro Arg Tyr Ile Arg
500 505 510

Val Leu Pro Glu Leu Pro Lys Thr Pro Thr Gly Lys Pro Thr Lys His
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Thr Leu Arg Ala Glu Gly Val Val Ala Gly Thr Trp Asp Arg Glu Ala
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Ala Gly Ile Arg Ile Arg Arg Glu Lys Ile Val
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28

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NEW_SEQLIST.ST25.txt

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34